AMENDMENTS TO THE SPECIFICATION

At page 31, line 1 of the specification following the claims, please insert the following new paragraph:

--Abstract of the Disclosure

SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3 encode an intracellular protein that is expressed in prostate epithelial cells in a hormone dependent manner. Encoded proteins SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:6 have predominantly perinuclear, nuclear and predominantly nuclear location localization within a cell, respectively. In contemplated methods of detecting a neoplastic cell in a system, a predetermined amount of at least one of SEQ ID NO:4, SEQ ID NO:5, and SEQ ID NO:5, or at least one of SEQ ID NO:7, SEQ ID NO:8, and SEQ ID NO:9 is correlated with the presence of a neoplastic cell and detected within the system employing specific binding of a labeled probe. In a method of identifying differentially expressed genes, a tissue specific array of cDNA prepared by suppression subtractive hybridization is arranged on a solid phase. Two nucleic acid preparations are individually hybridized with the array, wherein the first and second nucleic acid preparations are prepared from treated and untreated target tissue. A comparison of the hybridization patterns reveals differentially expressed genes.--

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At page 7, line 2, through page 8, line 3, please amend the paragraph as follows.

In a preferred embodiment, the system is a mammal (most preferably a human) and the neoplastic cell is a prostate cancer cell in a biopsy specimen. The total RNA is extracted from the biopsy specimen, and a real time quantitative RT-PCR ~~rt-PCR~~ employing individual reactions with primer pairs specific to each of the sequences of SEQ ID NO:15 – SEQ ID NO:21 is performed in parallel with a biopsy specimen known

to be free of cancer cells. Biopsy specimens are determined to have a cancer cell, where the detected mRNA quantity of SEQ ID NO:15 - SEQ ID NO:21 is at least 3 times higher than in the control specimen. A preferred extraction of total RNA utilizes the ~~Quiagen BioRobot~~ QIAGEN BioRobot® kit in conjunction with the ~~BioRobot~~ BioRobot® 9600 system, and the ~~real-time rtPCR~~ real-time RT-PCR is performed in a Perkin Elmer ABI ~~Prism~~ Prism® 7700.

At page 12, line 13-22, please amend the paragraph as follows.

cDNA derived from poly(A)+ RNA of 10 different normal human tissues were subtracted against normal human prostate cDNA using suppression subtraction hybridization (SSH) (Diatchenko, L., Lau, Y.-F-C., Campbell, A.P., Chenchik, A., Moqadam, F., Huang, B., Lukyanov, S., Luyanov, K., Gurskaya, N., Sverdlov, E.D., Siebert, P.D. (1996). *Proc. Natl. Acad. Sci.* USA 93, 6025-6030), and the resulting cDNA fragments were cloned into an appropriate vector. SSH was performed as described (Clontech ~~PCR-Select~~ PCR-Select™ Cloning Kit) using prostate poly(A)+ RNA against a pool of poly(A)+ RNA obtained from ten normal human tissues (heart, brain, placenta, lung, liver, skeletal muscle, kidney, spleen, thymus, and ovary). Upon secondary PCR amplification (12 cycles), reactions were extracted with phenol/chloroform and DNA was precipitated with EtOH.

At page 12, line 23-28, please amend the paragraph as follows.

The pellet was washed once with 70% EtOH. After drying, the DNA pellet was dissolved in 0.2xTE or dH_2O and cut with RsaI in a 20 ul reaction for 2 hrs at 37C to excise adaptors. After digestion, reactions were run on a 1.5 % agrose gel, with molecular size markers on one side, at 5 V/cm, 40 min. The adopter bands are excised and discarded, and cDNA bands were cut out and purified (~~QAIEX~~ QIAX® gel DNA purification kit) after running the gel backwards to concentrate the cDNA.

At page 12, line 29-31, please amend the paragraph as follows.

The purified DNA was subcloned into EcoRV-cut, dephosphorylated ~~pZERO~~ pZERO® vector from Invitrogen. DH10B electrocompetent cells (>10^{10} efficiency) were transformed with a 1/5 dilution of 1µl of the ligation mix.